

OIPE

#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/944,930

DATE: 09/20/2001

TIME: 13:58:04

Input Set : A:\PP16021.002 SEQLIST.TXT

Output Set: N:\CRF3\09202001\I944930.raw

ENTERED

4 <110> APPLICANT: Hageman, Robert V.  
5 Shirley, Bret A.  
6 Bajwa, Kamaljit K.  
8 <120> TITLE OF INVENTION: Stabilized FGF Formulations Containing  
9 Reducing Agents  
11 <130> FILE REFERENCE: PP16021.002  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/944,930  
C--> 13 <141> CURRENT FILING DATE: 2001-08-31  
13 <150> PRIOR APPLICATION NUMBER: 60/229,238  
14 <151> PRIOR FILING DATE: 2000-08-31  
16 <160> NUMBER OF SEQ ID NOS: 8  
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 146  
22 <212> TYPE: PRT  
23 <213> ORGANISM: Homo sapiens  
25 <400> SEQUENCE: 1  
26 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His  
27 1 5 10 15  
28 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu  
29 20 25 30  
30 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp  
31 35 40 45  
32 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser  
33 50 55 60  
34 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly  
35 65 70 75 80  
36 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu  
37 85 90 95  
38 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr  
39 100 105 110  
40 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser  
41 115 120 125  
42 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala  
43 130 135 140  
44 Lys Ser  
45 145  
48 <210> SEQ ID NO: 2  
49 <211> LENGTH: 146  
50 <212> TYPE: PRT  
51 <213> ORGANISM: Bos taurus  
53 <400> SEQUENCE: 2  
54 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His  
55 1 5 10 15  
56 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu  
57 20 25 30  
58 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp

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```

59          35          40          45
60 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
61          50          55          60
62 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
63 65          70          75          80
64 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
65          85          90          95
66 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
67          100          105          110
68 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
69          115          120          125
70 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
71          130          135          140
72 Lys Ser
73 145

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76 &lt;210&gt; SEQ ID NO: 3

77 &lt;211&gt; LENGTH: 155

78 &lt;212&gt; TYPE: PRT

79 &lt;213&gt; ORGANISM: Homo sapiens

81 &lt;400&gt; SEQUENCE: 3

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82 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
83 1          5          10          15
84 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
85          20          25          30
86 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
87          35          40          45
88 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
89          50          55          60
90 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
91 65          70          75          80
92 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
93          85          90          95
94 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
95          100          105          110
96 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
97          115          120          125
98 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
99          130          135          140
100 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
101 145          150          155

```

104 &lt;210&gt; SEQ ID NO: 4

105 &lt;211&gt; LENGTH: 155

106 &lt;212&gt; TYPE: PRT

107 &lt;213&gt; ORGANISM: Bos taurus

109 &lt;400&gt; SEQUENCE: 4

```

110 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
111 1          5          10          15
112 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
113          20          25          30

```

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114 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
115          35          40          45
116 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
117          50          55          60
118 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
119 65          70          75          80
120 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
121          85          90          95
122 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
123          100          105          110
124 Asn Thr Tyr Arg Ser Arg Lys Tyr Ser Ser Trp Tyr Val Ala Leu Lys
125          115          120          125
126 Arg Thr Gly Gln Tyr Lys Leu Gly Pro Lys Thr Gly Pro Gly Gln Lys
127          130          135          140
128 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
129 145          150          155
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 441
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (1)...(441)
141 <400> SEQUENCE: 5
142 ccc gcc ttg ccc gag gat ggc ggc agc ggc gcc ttc ccg ccc ggc cac 48
143 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
144 1          5          10          15
146 ttc aag gac ccc aag cgg ctg tac tgc aaa aac ggg ggc ttc ttc ctg 96
147 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
148          20          25          30
150 cgc atc cac ccc gac ggc cga gtt gac ggg gtc cgg gag aag agc gac 144
151 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
152          35          40          45
154 cct cac atc aag cta caa ctt caa gca gaa gag aga gga gtt gtg tct 192
155 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
156          50          55          60
158 atc aaa gga gtg tgt gct aac cgt tac ctg gct atg aag gaa gat gga 240
159 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
160 65          70          75          80
162 aga tta ctg gct tct aaa tgt gtt acg gat gag tgt ttc ttt ttt gaa 288
163 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
164          85          90          95
166 cga ttg gaa tct aat aac tac aat act tac cgg tca agg aaa tac acc 336
167 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
168          100          105          110
170 agt tgg tat gtg gca ctg aaa cga act ggg cag tat aaa ctt gga tcc 384
171 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
172          115          120          125
174 aaa aca gga cct ggg cag aaa gct ata ctt ttt ctt cca atg tct gct 432

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175 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
176      130                      135                      140
178 aag agc tga
179 Lys Ser *
180 145
183 <210> SEQ ID NO: 6
184 <211> LENGTH: 441
185 <212> TYPE: DNA
186 <213> ORGANISM: Bos taurus
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (1)...(441)
192 <400> SEQUENCE: 6
193 cca gcc cta cca gaa gat ggg ggg tcc ggg gcc ttc cca cca ggg cac 48
194 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
195 1      5      10      15
197 ttc aaa gat cca aaa cga cta tat tgt aaa aac ggg ggg ttc ttc cta 96
198 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
199      20      25      30
201 cga atc cac cca gat ggg cga gta gat ggg gta cga gaa aaa tcc gat 144
202 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
203      35      40      45
205 cca cac atc aaa cta caa cta caa gcc gaa gaa cga ggg gta gta tcc 192
206 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
207      50      55      60
209 atc aaa ggg gta tgt gcc aac cga tat cta gcc atg aaa gaa gat ggg 240
210 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
211 65      70      75      80
213 cga cta cta gcc tcc aaa tgt gta acc gat gaa tgt ttc ttc ttc gaa 288
214 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
215      85      90      95
217 cga cta gaa tcc aac aac tat aac acc tat cga tcc cga aaa tat tcc 336
218 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
219      100      105      110
221 tcc tgg tat gta gcc cta aaa cga acc ggg caa tat aaa cta ggg cca 384
222 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
223      115      120      125
225 aaa acc ggg cca ggg caa aaa gcc atc cta ttc cta cca atg tcc gcc 432
226 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
227      130      135      140
229 aaa tcc taa
230 Lys Ser *
231 145
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 468
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS

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Input Set : A:\PP16021.002 SEQLIST.TXT

Output Set: N:\CRF3\09202001\I944930.raw

241 &lt;222&gt; LOCATION: (1)...(468)

243 &lt;400&gt; SEQUENCE: 7

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244 atg gca gcc ggg agc atc acc acg ctg ccc gcc ttg ccc gag gat ggc 48
245 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
246 1 5 10 15
248 ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg 96
249 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
250 20 25 30
252 tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga 144
253 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
254 35 40 45
256 gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt 192
257 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
258 50 55 60
260 caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac 240
261 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
262 65 70 75 80
264 cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288
265 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
266 85 90 95
268 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336
269 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
270 100 105 110
272 aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ctg aaa 384
273 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
274 115 120 125
276 cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa 432
277 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
278 130 135 140
280 gct ata ctt ttt ctt cca atg tct gct aag agc tga 468
281 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser *
282 145 150 155

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285 &lt;210&gt; SEQ ID NO: 8

286 &lt;211&gt; LENGTH: 468

287 &lt;212&gt; TYPE: DNA

288 &lt;213&gt; ORGANISM: Bos taurus

290 &lt;220&gt; FEATURE:

291 &lt;221&gt; NAME/KEY: CDS

292 &lt;222&gt; LOCATION: (1)...(468)

294 &lt;400&gt; SEQUENCE: 8

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295 atg gca gcc ggg agc atc acc acg ctg cca gcc cta cca gaa gat ggg 48
296 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
297 1 5 10 15
299 ggg tcc ggg gcc ttc cca cca ggg cac ttc aaa gat cca aaa cga cta 96
300 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
301 20 25 30
303 tat tgt aaa aac ggg ggg ttc ttc cta cga atc cac cca gat ggg cga 144
304 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
305 35 40 45

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/944,930

DATE: 09/20/2001

TIME: 13:58:05

Input Set : A:\PP16021.002 SEQLIST.TXT

Output Set: N:\CRF3\09202001\I944930.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date